

#1

[NCBI](#)[Entrez](#)[BLAST 2 sequences](#)[BLAST](#)[Example](#)[Help](#)

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using [BLAST](#) engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#)
Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program Matrix Parameters used in [BLASTN](#) program only:Reward for a match: Penalty for a mismatch: ☐ Use [Mega BLAST](#) Strand option View option Masking character option Masking color option ☐ Show CDS translationOpen gap and extension gap penaltiesgap x_dropoff expect word size Filter ☒

Sequence 1

Enter accession, GI or sequence in FASTA format from: to:

```
gtgaacttttatgggaaggatgcttctgaaaaacaaatgacagaaaactctccgccaggg
gaatttttttctcaatttttgatgaataagaacgatttgaaaatacaatggttggtgtttt
tatcttttttagagagctaaagggtgcctagaatctcttttcaaaaagcagattctctcatg
ttttttttctttatttgggtgtcatattctttttacatcttctgaccacttatcctcaagt
tgtacctctcatgttttataatgacaagctggatcaacatgggaaaagggtgaactggca
gtgatttcaccagccctgacatccttgcattccaccagcgtgctcctttaagttcagccca
```

or upload FASTA file

Sequence 2

Enter accession, GI or sequence in FASTA format from: to:

```
gcaatattaacaggcagctgtcccttggttcccagatgctgggatgactcgcatgtgctg
agcgggtgtggtcactgccaaaggaatgacctctcacatttcttctgattcgcatagc
cgcgccagcttgatcatctccctcttgggttcccagacactaagtctggaatgaaaatt
cacctgctctgaattggccactgggtgggggcaggggtgtgacttggttcccaggctgg
aagattatctcaccagccctagctatataacgggctgggtgtggaggggctccacagggc
cagttccaggggttcattccacaagagagaaaaacata
```

or upload FASTA file [Comments and suggestions to blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.14 [May-07-2006]

Match: Mismatch: gap open: gap extension:

x_dropoff: 50 expect: 10.000 wordsize: 11 Filter ☒ View option Standard

Masking character option Masking color option

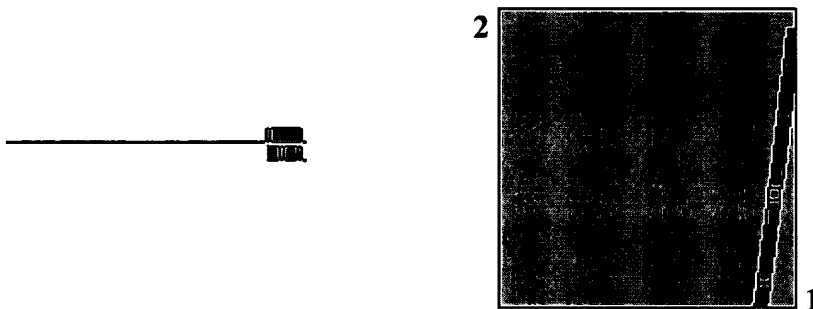
☐ Show CDS translation Align

Sequence 1: lcl|1_seq_1

Length = 2740 (1 .. 2740)

Sequence 2: lcl|2_seq_2

Length = 337 (1 .. 337)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

Score = 262 bits (136), Expect = 6e-66
Identities = 266/321 (82%), Gaps = 7/321 (2%)
Strand=Plus/Plus

[illegible]

9/25/06

[NCBI](#)[Entrez](#)[BLAST 2 sequences](#)[BLAST](#)[Example](#)[Help](#)

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Sequence 1

Enter accession, GI or sequence in FASTA format from: to:

```
gtgaacttttatgggaaggatgcttctgaaaaacaaatgacagaaaactctccgccaggg
gaatttttttctcaatttttgatgaataagaacgatttgaaaatacaatgggtgtgtgttt
tatcttttagagagctaaaggtgcctagatctctttcaaaaagcagattctctcatg
tttttttctttatttgtgtgcatattcttttacatctctgaccacttatcctcaagt
tgtacctctcatgttttataatgacaagctggatcaacatgggaaaagggtgaactggca
gtgatttcaccagccctgacatccttgcacccaccagcgtgctcctttaagttcagccca
```

or upload FASTA file

Sequence 2

Enter accession, GI or sequence in FASTA format from: to:

```
ggatcctttcatgtttaacaatatcaaccctaaccgaagggaacagcctgcctgacagt
ggctttgccacccatgaataacttcttagtctagtcggttgtaaactcagcccatccca
acacttctgcaagccccatcctctacaaggtgctcattgggaatttcttgagcttctct
ttcaggatcagcctgattctagggcagcagttctcaacctgggggcctcgaccctttgg
gggaatcaaacgaccctttacaggggtcacatatcatctatcctatatgtcaggtattta
cattacgattcgtaacagtagcaaaattacaggtatgaaatagcaatgaaataattttat
```

or upload FASTA file [Comments and suggestions to blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)



Blast 2 Sequences results

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BLAST

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Taxonomy

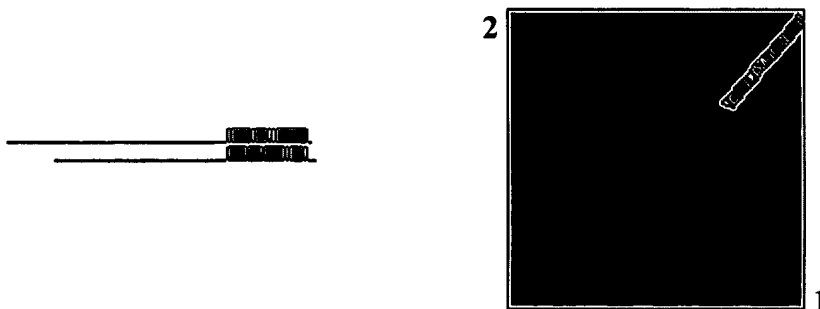
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.14 [May-07-2006]

Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: Filter ☒ View option
 Masking character option Masking color option
☐ Show CDS translation

Sequence 1: lcl|1_seq_1
 Length = 2740 (1 .. 2740)

Sequence 2: lcl|2_seq_2
 Length = 2358 (1 .. 2358)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

Score = 417 bits (217), Expect = 8e-113
 Identities = 561/699 (80%), Gaps = 20/699 (2%)
 Strand=Plus/Plus

Query	2034	TTTAGAACACGGTAAGCATGTCATGTGCTAAT---GGCCAGTGACATCATAAAAGAAAAG	2090
Sbjct	1597	TTTAGAACACGGTGAGCCTGTGGTGCACTAATTATGGCCAGTGACACCATAGAGTCAAAG	1656
Query	2091	TGCATTACTGAATGCTTTCAATTTCTTATAATGATGGTAAGGTGGCATGTCATGGGGCCT	2150
Sbjct	1657	TGCATTACTGAATGCTTTCAATTTCTCCTAATGCTGGTACGATGGCATGTCACAGGGCCA	1716
Query	2151	ATTTAGCCCCAGACATCACTCCAAAGAATTCCAAACAGATATAGACAAGTGCCTTTAGGG	2210

```

Sbjct  1717  TTTTAGCTGCAGACATCACTCCAGAGAATTCCAAACAGATAGAGACAAGTGGCACCCAGA 1776
Query  2211  CCCAGATCCCTTCCCCCTCAGGCTGTTTA-CCCAGGGAATAGGATGTCTGGGACAAGT-T 2268
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  1777  CCCATCTCC-TTCCCCCTCGGGCTGATTATCCCCAGAAATAGGATGTCCCAAAGCAACACT 1835
Query  2269  TCCC--CTAAGTGAAGTGTTGATAAGTCTGCCTTATCAGAAAGATATTACTGGGGGTGTGA 2326
      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  1836  TCCCAGCCAACTGGAGTGCTGATAAGTCCAGTTATCAGAAAGATATGGCTGTAAGTGTGA 1895
Query  2327  TATGTAGGGCATCTACATTTTCTTGATAGGT-AGTCATATGAAAGCTGACAAAGnnnnnn 2385
      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  1896  TGCACAGTGCTTG--CATTTTCTTGATACGTTAGTCATATGAGAGCTGACAAAGAAGGAA 1953
Query  2386  n--GGGCAGTGATGTGGTGCAATGTCAACAGACAGCTGTCCCCTGACT-CTTGACAAATA 2442
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  1954  AAAGAGCAGCGATGTGGTGCAATATTAACAGGCAGCTGTCCCCTGGCTTCCCAGATACGTG 2013
Query  2443  GGATGACTTGCATTGCTGAGCGATGTGATCACCACCAAAGGAATGGCCCTCTCACATTTTC 2502
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  2014  GGATGACTCGCATTGCTGAGCGGTGTGGTCACTGCCAAAGGAATGACCTCTCACATTTTC 2073
Query  2503  TTCCTGATTACATATTCAGCAGGGTTAGCTTGTCTCCCCCTCCCTCTTCAGCTTCCCAG 2562
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  2074  TTCCTGATTGCGATACGCCGC--GGCCAGCTTGTTCATC---TCCCTCTTGGGCTTCCCAG 2128
Query  2563  AACTGAGTCTGGAATGAAAATTCACCTGCCTCTGAGTTGGCTCCTAATGGGGGCGGGAG 2622
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  2129  AACTAAGTCTGGAATGAAAATTCACCTGCCTCTGAATTGGCCACTGGTGGGGGCGGGG 2188
Query  2623  TGTACTTTCGGTTCCCAGGTTGGAAGATTATCTCACCCGGCCCCAGCTATATAAGCTGAC 2682
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  2189  TGTGACTTGGCTTCCCAGGCTGGAAGATTATCTCACCCAGCCCTAGCTATATAA-CGGGC 2247
Query  2683  CGGTGTGGAGGGGCCAGCAGGGCCAACTCCAGGGATTC 2721
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  2248  TGGTGTGGAGGGGCTCCACAGGGCCAGTTCCAGGGGTTC 2286

```

CPU time: 0.02 user secs. 0.01 sys. secs 0.03 total secs.

Lambda K H
1.33 0.621 1.12

Gapped
Lambda K H
1.33 0.621 1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 1
Number of Hits to DB: 145
Number of extensions: 18
Number of successful extensions: 10
Number of sequences better than 10.0: 1
Number of HSP's gapped: 3
Number of HSP's successfully gapped: 1
Length of query: 2740

Length of database: 18,315,253,495
Length adjustment: 27
Effective length of query: 2713
Effective length of database: 18,315,253,468
Effective search space: 49689282658684
Effective search space used: 49689282658684
X1: 11 (21.1 bits)
X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 14 (27.6 bits)
S2: 22 (43.0 bits)